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(54) Title: INHIBITORS OF APOPTOSIS

(57) Abstract

The invention provides methods and compositions relating to novel human cellular inhibitor of apoptosis (c-IAP1/2) comprising a series of defined structural domain repeats and/or a RING finger domain; in particular, at least two of: a particular first domain repeat, a particular second domain repeat, and a particular third domain repeat, and/or a particular RING finger domain. The proteins provide a c-IAP specific function, with preferred proteins being capable of modulating the induction of apoptosis; for example, by binding a humain tumor necrosis factor receptor associated factor (TRAF). The compositions include nucleic acids which encode the subject c-IAP and hybridization probes and primers capable of hybridizing with the disclosed c-IAP genes. The invention includes methods of using the subject compositions in therapy, in diagnosis and in the biopharmaceutical industry.

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Inhibitors of Apoptosis

INTRODUCTION

Field of the Invention

The field of this invention is human proteins involved in the inhibition of apoptosis, or programmed cell death.

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Background

Cellular apoptosis, or programmed cell death, may be initiated by a variety of different stimuli including viral infection, certain cell-culture conditions, cell-cell signaling, cytokines, etc. Elucidation of signal transduction pathways leading to 10 apoptosis would provide valuable insight into a variety of pathogenic mechanisms. Accordingly, the ability to exogenously modulate the induction of apoptosis would yield therapeutic application for numerous clinical indications. In addition, components of such pathways would provide valuable targets for automated, cost-effective, high throughput drug screening and hence would have immediate 15 application in domestic and international pharmaceutical and biotechnology drug development programs.

Relevant Literature

Rothe *et al.* (1994) Cell 78, 681-692, report the existence of tumor necrosis 20 factor (TNF) receptor associated proteins which co-immunoprecipitate with a TNF receptor; see also Rothe, *et al.*, pending US patent application Serial No: 08/446,915. Roy, *et al.* (1995) Cell 80, 167-178 disclose the gene for a human neuronal apoptosis

inhibitory protein. Birnbaum et al. (1994) J Virol 68, 2521-2528 disclose an inhibitor of apoptosis (iap) gene, Op-iap from the Orgyia pseudotsugata nuclear polyhedrosis virus (OpMNPV) with sequence similarity to two other viral genes: Cp-iap derived from Cydia pomonella granulosis virus (CpGV), and iap derived from the Autographa californica nuclear polyhedrosis virus (AcMNPV). Clem and Miller (1994), in Apoptosis II: The Molecular Basis of Apoptosis in Disease, pp 89-110, Cold Spring Harbor Laboratory Press, provide a recent review of apoptosis regulation by insect viruses.

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SUMMARY OF THE INVENTION

The invention provides methods and compositions relating to novel human cellular inhibitor of apoptosis proteins (c-IAP). The subject proteins comprise a series of defined structural domain repeats and/or a RING finger domain; in particular, at least two of a first domain repeat comprising SEQUENCE ID NO: 5 or 6; a second domain repeat comprising SEQUENCE ID NO: 7 or 8; and a third domain repeat comprising SEQUENCE ID NO: 9 or 10; and/or a RING finger domain comprising SEQUENCE ID NO: 11 or 12, or a consensus sequences derived from these human genes. The proteins provide a c-IAP specific function, with preferred proteins being capable of modulating the induction of apoptosis; for example, by binding a human tumor necrosis factor receptor associated factor, TRAF. The compositions include nucleic acids which encode the subject c-IAP and hybridization probes and primers capable of hybridizing with the disclosed c-IAP genes.

The invention includes methods of using the subject compositions in therapy (e.g. gene therapy to enhance expression of a c-IAP gene), in diagnosis (e.g. genetic hybridization screens for c-IAP gene mutations, and in the biopharmaceutical industry (e.g. reagents for increasing yields of recombinant protein by enhancing host cell survival in culture, for screening chemical libraries for lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease associated with apoptosis regulation, etc.).

30

DETAILED DESCRIPTION OF THE INVENTION

The invention provides methods and compositions relating to novel cellular inhibitor of apoptosis proteins (c-IAPs). The nucleotide sequence of a natural cDNA encoding human c-IAP is shown as SEQUENCE ID NO:1 and the full conceptual translate is shown as SEQUENCE ID NO:2. The nucleotide sequence of another 5 natural cDNA encoding human c-IAP2 is shown as SEQUENCE ID NO:3 and the full conceptual translate is shown as SEQUENCE ID NO:4. The human c-IAPs of the invention include incomplete translates of SEQUENCE ID NOS:1 and 3 or deletion mutants of SEQUENCE ID NOS: 2 and/or 4, which translates or deletions mutants have at least one of the human c-IAP specific activities described herein. In addition, 10 the invention provides nonhuman mammalian homologs of the disclosed human c-IAPs. These homologs are encoded by natural cDNAs which are capable of specifically hybridizing with one or more of the disclosed human cDNAs under hybridization conditions describe below and are isolated using the methods and reagents described herein. For example, the amino acid sequence of a murine 15 homolog of c-IAP1, and the sequence its cDNA are shown in SEQUENCE ID NOS: 14 and 13.

The subject proteins comprise a series of defined structural domain repeats and/or a RING finger domain shown to be necessary for human c-IAP specific function; generally including at least two of: a first domain repeat comprising 20 SEQUENCE ID NO: 5, 6 or a consensus of 5 and 6, a second domain repeat comprising SEQUENCE ID NO: 7, 8 or a consensus of 7 and 8, and a third domain repeat comprising SEQUENCE ID NO: 9, 10 or a consensus of 9 and 10; and/or a RING finger domain comprising SEQUENCE ID NO: 11, 12 or a consensus of 11 and 12. Preferred domain repeat containing c-IAPs contain each of the three domain 25 repeats. More preferred c-IAPs comprise the three domain repeats and the C-terminal RING finger. To secure or optimize the requisite function for the protein, the repeats are usually preceded (N-terminally) and separated by intervening regions of about 10 to about 100 residues, which regions preferably derive from those found in the natural c-IAP1 and c-IAP2 translates. Similarly, the RING finger domain of RING finger 30 domain containing c-IAPs containing proteins is usually preceded by an N-terminal region of about 10 to 300 residues, usually 100 to 300 residues, which region preferably derives from those found in the natural c-IAP1 and c-IAP2 translates.

The proteins provide a human c-IAP1 or c-IAP2 (c-IAP1/2) specific activity or function which may be determined by convenient in vitro, cell-based, or in vivo assays. Preferred proteins are capable of modulating the induction of apoptosis. Such activity or function may be demonstrated in cell culture (e.g. cell transfections) or in animals (e.g. in vivo gene therapy, transgenics). c-IAP1/2 specific function can also be demonstrated by specific binding to a c-IAP1/2 specific binding target, including natural binding targets and nonnatural targets such as c-IAP1/2 specific antibodies. For example, c-IAPs comprising at least two of SEQUENCE ID NOS: 6, 7 and 8 are capable of specifically binding human tumor necrosis factor receptor associated factors 1 and 2 (TRAF1 and TRAF2) in simple in vitro binding assays. Finally, specific function can be assayed immunologically by the ability of the subject protein to elicit a c-IAP1/2 specific antibody in a rodent or rabbit. Generally, human c-IAP1/2-specificity of the binding agent is shown by binding equilibrium constants (usually at least about 10^7 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}). A wide variety of cell-based and cell-free assays may be used to demonstrate human c-IAP1/2-specific binding; preferred are rapid in vitro, cell-free assays such as mediating or inhibiting human c-IAP1/2-protein (e.g. human c-IAP1-TRAF2) binding, immunoassays, etc.

The claimed human c-IAP proteins are isolated, partially pure or pure and are typically recombinantly produced. An "isolated" protein for example, is unaccompanied by at least some of the material with which it is associated in its natural state and constitutes at least about 2%, and preferably at least about 5% by weight of the total protein in a given sample; a partially pure protein constitutes at least about 10%, preferably at least about 30%, and more preferably at least about 60% by weight of the total protein in a given sample; and a pure protein constitutes at least about 70%, preferably at least about 90%, and more preferably at least about 95% by weight of the total protein in a given sample. A wide variety of molecular and biochemical methods are available for generating and expressing the subject compositions, see e.g. Molecular Cloning, A Laboratory Manual (Sambrook, et al. Cold Spring Harbor Laboratory), Current Protocols in Molecular Biology (Eds. Ausubel, et al., Greene Publ. Assoc., Wiley-Interscience, NY) or that are otherwise known in the art..

The invention provides human c-IAP1/2-specific binding agents including substrates, natural intracellular binding targets, etc., and methods of identifying and making such agents, and their use in diagnosis, therapy and pharmaceutical development. For example, human c-IAP1/2-specific agents are useful in a variety of diagnostic and therapeutic applications, especially where disease or disease prognosis is associated with improper utilization of a pathway involving human c-IAP1/2, e.g. apoptosis. Novel human c-IAP1/2-specific binding agents include human c-IAP1/2-specific antibodies and other natural intracellular binding agents identified with assays such as one- and two-hybrid screens, non-natural intracellular binding agents identified in screens of chemical libraries, etc.

The invention also provides nucleic acids encoding the subject proteins, which nucleic acids may be part of human c-IAP1/2-expression vectors and may be incorporated into recombinant cells for expression and screening, transgenic animals for functional studies (e.g. the efficacy of candidate drugs for disease associated with c-IAP1/2 mediated signal transduction), etc., and nucleic acid hybridization probes and replication/amplification primers having a human c-IAP1/2 cDNA specific sequence contained in SEQUENCE ID NO:1 or 3. Nucleic acids encoding human c-IAP1/2 are isolated from eukaryotic cells, preferably human cells, by screening cDNA libraries with probes or PCR primers derived from the disclosed human c-IAP1/2 cDNA.

In addition, the invention provides nucleic acids sharing sufficient sequence similarity with that of the disclosed human c-IAP1/2 cDNAs to effect hybridization thereto. Such human c-IAP1/2 cDNA homologs are capable of hybridizing to the human c-IAP1/2-encoding nucleic acid defined by SEQUENCE ID NO: 1 or 3 under stringency conditions characterized by a hybridization buffer comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M NaPO₄, pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with the 0.2 x SSPE. Preferred nucleic acids will hybridize in a hybridization buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remain bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C. Human c-IAP1/2 cDNA homologs can also be characterized by BLASTX (Altschul et al. (1990) Basic Local Alignment Search Tool, J Mol Biol 215, 403-410) probability scores. Using this nucleic acid sequence search program BLASTX, complete coding

region human c-IAP1/2 cDNA homologs provide a Probability P(N) score of less than 1.0e-200. More preferred nucleic acids encode c-IAPs with at least about 50%, preferably at least about 60%, more preferably at least 70% pair-wise identity to at least one of SEQUENCE ID NOS: 2 and 4.

5 The subject nucleic acids are isolated, i.e. constitute at least about 0.5%, preferably at least about 5% by weight of total nucleic acid present in a given fraction. The subject nucleic acids find a wide variety of applications including use as translatable transcripts, hybridization probes, PCR primers, therapeutic nucleic acids, etc.; use in detecting the presence of human c-IAP1/2 genes and gene transcripts, in
10 detecting or amplifying nucleic acids encoding additional human c-IAP1/2 homologs and structural analogs, and in gene therapy applications. When used as expression constructs, the nucleic acids are usually recombinant, meaning they comprise a sequence joined to a nucleotide other than that which it is joined to on a natural chromosome. The subject nucleic acids may be contained within vectors, cells or
15 organisms.

In diagnosis, c-IAP1/2 hybridization probes find use in identifying wild-type and mutant c-IAP1/2 alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses. In therapy, therapeutic c-IAP1/2 nucleic acids are used to modulate
20 cellular expression or intracellular concentration or availability of active c-IAP1/2. A wide variety of indications may be treated, either prophylactically or therapeutically with the subject compositions. For example, where cell-specific apoptosis or other limitation of cell growth is desired, e.g. neoproliferative disease, a reduction in c-IAP1/2 expression is effected by introducing into the targeted cell type c-IAP1/2
25 nucleic acids which reduce the functional expression of c-IAP1/2 gene products (e.g. nucleic acids capable of inhibiting translation of a c-IAP1/2 protein). Conditions for treatment include restenosis, where vascular smooth muscle cells are involved, inflammatory disease states, where endothelial cells, inflammatory cells and glomerular cells are involved, myocardial infarction, where heart muscle cells are
30 involved, glomerular nephritis, where kidney cells are involved, transplant rejection where endothelial cells are involved, infectious diseases such as HIV infection where certain immune cells and other infected cells are involved, or the like.

These c-IAP1/2 inhibitory nucleic acids are typically antisense: single-stranded sequences comprising complements of the disclosed c-IAP1/2 encoding nucleic acid.

Antisense modulation of the expression of a given c-IAP1/2 protein may employ c-IAP1/2 antisense nucleic acids operably linked to gene regulatory sequences. Cell

5 are transfected with a vector comprising a c-IAP1/2 sequence with a promoter sequence oriented such that transcription of the gene yields an antisense transcript capable of binding to endogenous c-IAP1/2 protein encoding mRNA. Transcription of the antisense nucleic acid may be constitutive or inducible and the vector may provide for stable extrachromosomal maintenance or integration. Alternatively, single-

10 stranded antisense nucleic acids that bind to genomic DNA or mRNA encoding a given c-IAP1/2 protein may be administered to the target cell, in or temporarily isolated from a host, at a concentration that results in a substantial reduction in expression of the targeted protein.

In other indications, e.g. certain hypersensitivities, atrophic diseases, etc., a reduction in apoptosis is desired. In these applications, an enhancement in c-IAP1/2 expression is effected by introducing into the targeted cell type c-IAP1/2 nucleic acids which increase the functional expression of c-IAP1/2 gene products. Conditions for treatment include multiple sclerosis, where certain neuronal cells are involved, inflammatory disease states such as rheumatoid arthritis, where bystander cells are involved, transplant rejection where graft cells are involved, infectious diseases such as HIV infection where certain uninfected host cells are involved, or the like. Such nucleic acids may be c-IAP1/2 expression vectors, vectors which upregulate the functional expression of an endogenous c-IAP1/2 allele, or replacement vectors for targeted correction of c-IAP1/2 mutant alleles.

25 Various techniques may be employed for introducing of the nucleic acids into viable cells. The techniques vary depending upon whether one is using the subject compositions in culture or *in vivo* in a host. Various techniques which have been found efficient include transfection with a retrovirus, viral coat protein-liposome mediated transfection, see Dzau et al., *Trends in Biotech* 11, 205-210 (1993). In some

30 situations it is desirable to provide the nucleic acid source with an agent which targets the target cells, such as an antibody specific for a surface membrane protein on the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are

employed, proteins which bind to a surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g., capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and 5 enhance intracellular half-life. In liposomes, the nucleic acid concentration in the lumen will generally be in the range of about 0.01 μM to 10 μM. For other techniques, the concentration and application rate is determined empirically, using conventional techniques to determine desired ranges.

- Application of the subject therapeutics may be systemic or local, i.e.
- 10 administered at the site of interest. Various techniques can be used for providing the subject compositions at the site of interest, such as injection, use of catheters, trocars, projectiles, pluronic gel, stents, sustained drug release polymers or other device which provides for internal access. Where an organ or tissue is accessible because of removal from the patient, such organ or tissue may be bathed in a medium containing 15 the subject compositions, the subject compositions may be painted onto the organ, or may be applied in any convenient way. Systemic administration of the nucleic acid may be effected using naked DNA, lipofection, liposomes with tissue targeting (e.g. antibody).

The invention provides methods and compositions for enhancing the yield of 20 many recombinantly produced proteins, such as tissue plasminogen activator (t-PA), by increasing maximum cell densities and survival time of host production cells in culture. Specifically, cultured cells are transfected with nucleic acids which effect the up-regulation of endogenous c-IAP or the expression of an exogenous c-IAP. For example, nucleic acids encoding functional c-IAP operably linked to a transcriptional 25 promoter are used to over-express the exogenous c-IAP in the host cell (see, experimental section, below). Such transformed cells demonstrate enhanced survival ability at elevated cell densities and over extended culture periods.

The invention provides efficient methods of identifying pharmacological agents or lead compounds for agents active at the level of a human c-IAP1/2 30 modulatable cellular function, particularly human c-IAP1/2 mediated signal transduction, especially in apoptosis. Generally, these screening methods involve assaying for compounds which modulate a human c-IAP1/2 interaction with a natural

c-IAP1/2 binding target. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for lead compounds. Identified reagents find use in the pharmaceutical industries for animal and human trials; for example, the reagents may be derivatized and rescreened in in vitro and in vivo assays to optimize 5 activity and minimize toxicity for pharmaceutical development. Target indications may include infection, genetic disease, cell growth and regulatory dysfunction, such as neoplasia, inflammation, hypersensitivity, etc.

A wide variety of assays for binding agents are provided including protein-protein binding assays, immunoassays, cell based assays, etc. The human c-IAP1/2 10 compositions used the methods are usually added in an isolated, partially pure or pure form and are typically recombinantly produced. The human c-IAP1/2 may be part of a fusion product with another peptide or polypeptide, e.g. a polypeptide that is capable of providing or enhancing protein-protein binding, stability under assay conditions (e.g. a tag for detection or anchoring), etc. The assay mixtures comprise a natural 15 intracellular human c-IAP1/2 binding target such as a TRAF. While native binding targets may be used, it is frequently preferred to use portions (e.g. peptides, nucleic acid fragments) thereof so long as the portion provides binding affinity and avidity to the subject human c-IAP1/2 conveniently measurable in the assay. The assay mixture also comprises a candidate pharmacological agent. Candidate agents encompass 20 numerous chemical classes, though typically they are organic compounds; preferably small organic compounds and are obtained from a wide variety of sources including libraries of synthetic or natural compounds. A variety of other reagents may also be included in the mixture. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal binding and/or 25 reduce non-specific or background interactions, etc. Also, reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, antimicrobial agents, etc. may be used.

The resultant mixture is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, the human c-IAP1/2 specifically 30 binds the cellular binding target, portion or analog with a reference binding affinity. The mixture components can be added in any order that provides for the requisite bindings. Incubations may be performed at any temperature which facilitates optimal

binding, typically between 4 and 40°C, more commonly between 15° and 40°C. Incubation periods are likewise selected for optimal binding but also minimized to facilitate rapid, high-throughput screening, and are typically between .1 and 10 hours, preferably less than 5 hours, more preferably less than 2 hours.

- 5 After incubation, the agent-influenced binding between the human c-IAP1/2 and one or more binding targets is detected by any convenient way. For cell-free binding type assays, a separation step is often used to separate bound from unbound components. Separation may be effected by precipitation (e.g. TCA precipitation, immunoprecipitation, etc.), immobilization (e.g. on a solid substrate), etc., followed by
10 washing by, for example, membrane filtration (e.g. Whatman's P-81 ion exchange paper, Polyfiltronic's hydrophobic GFC membrane, etc.), gel chromatography (e.g. gel filtration, affinity, etc.). In addition, one of the components usually comprises or is coupled to a label. A wide variety of labels may be employed - essentially any label that provides for detection of bound protein. The label may provide for direct
15 detection as radioactivity, luminescence, optical or electron density, etc. or indirect detection such as an epitope tag, an enzyme, etc. A variety of methods may be used to detect the label depending on the nature of the label and other assay components. For example, the label may be detected bound to the solid substrate or a portion of the bound complex containing the label may be separated from the solid substrate, and
20 thereafter the label detected. Labels may be directly detected through optical or electron density, radiative emissions, nonradiative energy transfers, etc. or indirectly detected with antibody conjugates, etc. For example, in the case of radioactive labels, emissions may be detected directly, e.g. with particle counters or indirectly, e.g. with scintillation cocktails and counters.

- 25 The following experiments and examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

- The murine cellular inhibitor of apoptosis protein 1 (c-IAP1) was
30 biochemically purified as a TNF-R2 associated protein using coimmunoprecipitation Rothe et al. (1994) supra. A large scale protein purification protocol provided material sufficient for peptide sequencing. Fully degenerate oligonucleotides corresponding to

two of the isolated peptides were used to specifically amplify a 0.75 kb DNA fragment from mouse CT6 RNA by Reverse Transcription-PCR. This DNA fragment was used to isolate full-length cDNA clones from a mouse CT6 cDNA library by hybridization (50% formamide, 5xSSPE, 42°C; filters washed at 42°C with 0.2XSSPE, where 5 1xSSPE is 0.18 M NaCl, 0.01 M NaPO₄, pH7.7, 0.001 M EDTA).

DNA sequence analysis predicted an open reading frame encoding a 612 amino acid protein that shows significant sequence similarity (36 % amino acid identity) with the 'inhibitor of apoptosis protein' (IAP) from insect viruses (Clem, R. J. and Miller, L. K., 1994, *supra*) and the human 'neuronal apoptosis inhibitory protein' (NAIP) (23 % 10 amino acid identity), that is involved in spinal muscular atrophy (SMA) an inherited disease in humans (Roy et al., 1995, *supra*). To obtain the human c-IAP1 gene, the originally amplified mouse DNA fragment was used as a probe to screen a HeLa cDNA library (30% formamide, 5xSSPE, 42°C; filters washed at 42°C with 0.2xSSPE). Sequence analysis of the isolated cDNA clones revealed that they 15 correspond to two distinct genes, designated c-IAP1 and c-IAP2. The human c-IAP1 cDNA encodes a protein of 618 amino acids that is 84% identical to murine c-IAP1. The human c-IAP2 cDNA encodes a protein of 604 amino acids that shares a high degree of amino acid identity with both murine and human c-IAP1 (72% and 73%, respectively) and represents another member of the IAP superfamily.

20 Comparison of the amino acid sequence of members of the IAP superfamily reveals that they are comprised of at least three distinct domains. The N-terminal region of all IAP family members is comprised of 'baculovirus IAP repeat' (BIR) motifs (Birnbaum et al., 1994, *supra*). While the viral proteins contain two repeats, the mammalian homologs (c-IAP1, -2) possess three BIR motifs. Similarly, NAIP 25 contains three BIR repeats. In addition to BIR motifs viral IAPs contain a C-terminal RING finger motif. This Zn-binding domain is also present in c-IAP1 and -2 but not in NAIP. Thus c-IAP1 and -2 define a distinct subfamily within the IAP superfamily that contain three BIR motifs and a RING finger motif. A RING finger domain is also present at the N-terminus of TRAF2 and has been shown to be involved in TRAF2 30 signal transduction. The RING finger motifs of c-IAP1 and -2 share significant sequence homology with the RING finger domains of viral IAPs but no homology with the TRAF2 RING finger domain besides the conserved cysteine and histidine

residues. The region between the BIR domain and the RING finger domain of c-IAP1 and -2 is strongly conserved but does not reveal any significant homology to other members of the IAP family or any other proteins in the NCBI database.

- A yeast two-hybrid system was used to determine how c-IAP1 and -2 interact
- 5 with TNF-R2 and/or TRAFs. The following results were obtained indistinguishably for c-IAP1 and c-IAP2. Two-hybrid analysis revealed that c-IAP1 does not directly interact with TNF-R2. However, a direct interaction could be detected between c-IAP1 and TRAF2. The conserved TRAF domain of TRAF2 (amino acids 264-501) is sufficient to mediate this interaction. Consistently, c-IAP1 also interacted with
- 10 TRAF1. Further analysis demonstrated that the coiled-coil region within the TRAF domain of TRAF2 (amino acids 251-358) is required for interaction with c-IAP1. In contrast, the C-terminal region of the TRAF domain (amino acids 359-501) that mediates the association of TNF-R2 with TRAF2 is dispensable for interaction of c-IAP1 with TRAF2. Thus c-IAP1 and TNF-R2 bind to non-overlapping docking
- 15 sites within the TRAF domain of TRAF2. Consistently, c-IAP1 does not interact with TRAF3 (e.g. Cheng et al. (1995), *supra*), which does not contain a coiled-coil region with sequence similarity to TRAF2/TRAF1. Deletion mutagenesis of c-IAP1 indicated that the N-terminal half of the protein containing the three BIR motifs (amino acids 1-336 of c-IAP1 and 1-396 of c-IAP2) is sufficient for interaction with
- 20 TRAF2 and TRAF1. Similarly, combinations of two of the three BIR motifs e.g. amino acid residues 46-99 and 204-249 of c-IAP1 and 29-82 and 189-234 of c-IAP2, separated by IAP1 derived intervening sequences of varying lengths are assayed for TRAF1 and TRAF2 binding. This indicates that BIR motifs represent a novel protein:protein interaction domain. The RING finger domain of c-IAP1/2 (amino acids
- 25 571-618 of c-IAP1 and 557-604 of c-IAP2) is not required for interaction with TRAFs, but rather mediates subsequent steps in the c-IAP1/2 signaling cascade. Similarly, a variety of c-IAP1 derived N-terminal leader sequences fused to the c-IAP1 RING finger domain are used to assay signal transduction mediation. In an analogous situation, the RING finger domain of TRAF2 has been demonstrated to be required for
- 30 TRAF2-mediated activation of NF- κ B.

A transfection based co-immunoprecipitation assay was used to investigate how c-IAP1 interacts with the complex of TNF-R2 and TRAFs. In this system c-IAP1

was N-terminally tagged with a FLAG epitope peptide and expressed in human embryonic 293 cells under the control of a constitutive CMV promotor (pRK vector).

The c-IAP1 expression vector was transiently co-transfected into 293 cells with expression vectors for TNF-R2 and TRAFs. After 24-36 h, the cells were harvested 5 and extracts immunoprecipitated with anti-TNF-R2 antibodies, followed by Western analysis with anti-FLAG antibodies. This assay demonstrated that while c-IAP1 associates directly with TRAF1 and TRAF2, its interaction with TNF-R2 is indirect and requires the heterocomplex of TRAF1 and TRAF2. Thus, c-IAP1 is a component of the TNF-R2 (CD40)/TRAF signaling complex.

10 To determine the functional properties of c-IAP1 transient transfection assays were performed in human rhabdomyosarcoma KYM1 cells. The results indicate that overexpression of c-IAP1 but not of control vector, TRAF1 or TRAF2 protects KYM1 cells from TNF-induced programmed cell death (apoptosis). Hence, c-IAP1 regulates the cellular response to TNF by modulating TNF responsiveness, e.g. the initiation of 15 an apoptotic or protective program. The transient transfection assay also finds use as a drug screening assay. In this application, candidate agents are screened as above for their ability to modulate the ability of c-IAP1 to downregulate apoptosis.

EXAMPLES

20 1. Protocol for human c-IAP1 - TRAF2 binding assay.

A. Reagents:

- Neutralite Avidin: 20 µg/ml in PBS.

- Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.

25 - Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 0.25 mM EDTA, 1% glycerol, 0.5% NP-40, 50 mM β-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors.

- ³²P human c-IAP1 10x stock: 10⁻⁸ - 10⁻⁶ M unlabeled human c-IAP1 supplemented with 200,000-250,000 cpm of labeled human c-IAP1/21 (Beckman counter).

30 Place in the 4°C microfridge during screening.
- Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506).

25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVO₃ (Sigma # S-6508) in 10 ml of PBS.

- TRAF2: 10⁻⁸ - 10⁻⁵ M biotinylated truncated TRAF2 (residues 264-501) in PBS.

5 B. Preparation of assay plates:

- Coat with 120 µl of stock N-Avidin per well overnight at 4°C.
- Wash 2 times with 200 µl PBS.
- Block with 150 µl of blocking buffer.
- Wash 2 times with 200 µl PBS.

10 C. Assay:

- Add 40 µl assay buffer/well.
- Add 10 µl compound or extract.
- Add 10 µl ³³P-human c-IAP1 (20,000-25,000 cpm/0.1-10 pmoles/well = 10⁻⁹ 10⁻⁷ M final concentration).

15 - Shake at 25°C for 15 minutes.

- Incubate additional 45 minutes at 25°C.
- Add 40 µl biotinylated truncated TRAF2 (0.1-10 pmoles/40 µl in assay

buffer)

- Incubate 1 hour at room temperature.

20 - Stop the reaction by washing 4 times with 200 µl PBS.

- Add 150 µl scintillation cocktail.

- Count in Topcount.

D. Controls for all assays (located on each plate):

a. Non-specific binding

25 b. Soluble (non-biotinylated truncated TRAF2) at 80% inhibition.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes

and modifications may be made thereto without departing from the spirit or scope of
the appended claims.

	SEQUENCE ID NO: 1, 2	h (human) c-IAP1	cDNA, protein
5	SEQUENCE ID NO: 3, 4	h c-IAP2	cDNA, protein
	SEQUENCE ID NO: 5, 6	h c-IAP1,2 repeat 1	protein, protein
	SEQUENCE ID NO: 7, 8	h c-IAP1,2 repeat 2	protein, protein
	SEQUENCE ID NO: 9, 10	h c-IAP1,2 repeat 3	protein, protein
	SEQUENCE ID NO: 11, 12	h c-IAP1,2 RING finger	protein, protein
10	SEQUENCE ID NO: 13, 14	m (murine) c-IAP	cDNA, protein

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TULARIK, INC.
- (ii) TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 - (B) STREET: 4 Embarcadero Center, Suite 3400
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US96/
 - (B) FILING DATE: 06 AUG 1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBERS: U.S. Serial Nos. 08/512,946 & 08/569,749
 - (B) FILING DATES: 08 AUG 1995 & 08 DEC 1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brezner, David J.
 - (B) REGISTRATION NUMBER: 24,774
 - (C) REFERENCE/DOCKET NUMBER: A-62464/DJB
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 781-1989
 - (B) TELEFAX: (415) 398-3249

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAAGTAGT ATCTTGAAA TTCAGAGAGA TACTCATCCT ACCTGAATAT AAACGTGAGAT	60
AAATCCAGTA AAGAAAGTGT AGTAAATTCT ACATAAGAGT CTATCATTGA TTTCTTTTGG	120
TGGTAAAAAT CTTAGTCAT GTGAAGAAAAT TTCAATGTGAA TGTTTTAGCT ATCAAACAGC	180
ACTGTCACCT ACTCATGCAC AAAACTGCCT CCCAAAGACT TTTCCCAGGT CCCTCGTATC	240
AAAACATTAAGT GAGTATAATG GAAGATAGCA CGATCTTGTC AGATGGACA AACAGCAACA	300

AACAAAAAAAT	GAAGTATGAC	TTTCCTGTG	AACTCTACAG	AATGTCTACA	TATTCAACTT	360
TCCCCGCCGG	GGTGCCTGTC	TCAGAAAGGA	GTCTTGCTCG	TGCTGGTTT	TATTATACTG	420
GTGTGAATGA	CAAGGTCAAA	TGCTTCTGTT	GTGGCCTGAT	GCTGGATAAC	TGGAAACTAG	480
GAGACAGTCC	TATTCAAAAG	CATAAACAGC	TATATCCTAG	CTGTAGCTT	ATTCAAGAAC	540
TGGTTTCAGC	TAGTCTGGGA	TCCACCTCTA	AGAATACGTC	TCCAATGAGA	AACAGTTTG	600
CACATTCACTT	ATCTCCCACC	TTGGAACATA	GTAGCTTGT	CAGTGGTTCT	TACTCCAGCC	660
TTTCTCCAAA	CCCTCTTAAT	TCTAGAGCAG	TTGAAGACAT	CTCTTCATCG	AGGACTAAC	720
CCTACAGTTA	TGCAATGAGT	ACTGAAGAAG	CCAGATTTCT	TACCTACCAT	ATGTGGCCAT	780
TAACTTTTT	GTCACCATCA	GAATTGGCAA	GAGCTGGTTT	TTATTATATA	GGACCTGGAG	840
ATAGGGTAGC	CTGCTTGCC	TGTGGTGGGA	AGCTCAGTAA	CTGGGAACCA	AAGGATGATG	900
CTATGTCAGA	ACACCGGAGG	CATTTCCCA	ACTGTCCATT	TTTGGAAAAT	TCTCTAGAAA	960
CTCTGAGGTT	TAGCATTCA	AATCTGAGCA	TGCAGACACA	TGCAGCTCGA	ATGAGAACAT	1020
TTATGTACTG	GCCATCTAGT	GTTCCAGTTC	AGCCTGAGCA	GCTTGCAAGT	GCTGGTTTT	1080
ATTATGTGGG	TCGCAATGAT	GATGTCAAAT	GCTTTGTTG	TGATGGTGGC	TTGAGGTGTT	1140
GGGAATCTGG	AGATGATCCA	TGGGTAGAAC	ATGCCAAGTG	GTTCCAAGG	TGTGAGTTCT	1200
TGATACGAAT	GAAAGGCCAA	GAGTTGTTG	ATGAGATTCA	AGGTAGATAT	CCTCATCTTC	1260
TTGAACAGCT	GTTGTCAACT	TCAGATAACCA	CTGGAGAAGA	AAATGCTGAC	CCACCAATT	1320
TTCATTTGG	ACCTGGAGAA	AGTTCTTCAG	AAGATGCTGT	CATGATGAAT	ACACCTGTGG	1380
TTAAATCTGC	CTTGGAAATG	GGCTTTAATA	GAGACCTGGT	GAAACAAACA	GTTCAAAGTA	1440
AAATCCTGAC	AACTGGAGAG	AACTATAAAA	CAGTTAATGA	TATTGTGTCA	GCACCTCTAA	1500
ATGCTGAAGA	TGAAAAAAGA	GAGGAGGAGA	AGGAAAACAA	AGCTGAAGAA	ATGGCATCAG	1560
ATGATTTGTC	ATTAATTCCG	AAGAACAGAA	TGGCTCTCTT	TCAACATTG	ACATGTGTGC	1620
TTCCTATCCT	GGATAATCTT	TTAAAGGCCA	ATGTAATTAA	TAAACAGGAA	CATGATATTA	1680
TTAAACAAAAA	AAACACAGATA	CCTTACAAG	CGAGAGAACT	GATTGATACC	ATTITGGTTA	1740
AAGGAAATGC	TGCGGCCAAC	ATCTTCAAAA	ACTGTCTAAA	AGAAATTGAC	TCTACATTGT	1800
ATAAGAACTT	ATTTGTGGAT	AAGAATATGA	AGTATATTCC	AACAGAAGAT	GTTCAGGTC	1860
TGTCACTGGA	AGAACAAATTG	AGGAGGTTGC	AAGAAGAACG	AACTGTAAA	GTGTGTATGG	1920
ACAAAGAAGT	TTCTGTTGTA	TTTATTCTT	GTGGTCATCT	GGTAGTATGC	CAGGAATGTG	1980
CCCCTTCTCT	AAGAAAATGC	CCTATTGCA	GGGGTATAAT	CAAGGGTACT	GTTCGTACAT	2040
TTCTCTCTTA	AAGAAAATA	GTCTATATTT	TAACCTGCAT	AAAAAGGTCT	TTAAAATATT	2100
GTTGAACACT	TGAAGCCATC	TAAAGTAAAAA	AGGGAATTAT	GAGTTTTCA	ATTAGTAACA	2160
TTCATGTTCT	AGTCTGCTTT	GGTACTAATA	ATCTTGTTC	TGAAAAGATG	GTATCATATA	2220
TTTAATCTTA	ATCTGTTAT	TTACAAGGGA	AGATTTATGT	TTGGTGAACT	ATATTAGTAT	2280
GTATGTGTAC	CTAAGGGAGT	AGTGTCACTG	CTTGTATGC	ATCATTTCAG	GAGTTACTGG	2340

ATTTGTTGTT CTTTCAGAAA GCTTTGAATA CTAATTATA GTGTAGAAAAA GAACTGGAAA	2400
CCAGGAACTC TGGAGTTCAT CAGAGTTATG GTGCCGAATT GTCTTGTTG CTTTCACTT	2460
GTGTTTAAA ATAAGGATT TTCTCTTATT TCTCCCCCTA GTTTGTGAGA AACATCTCAA	2520
TAAAGTGCTT TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2580
AAAAAAAAA	2589

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Ser Tyr Gln	
1 5 10 15	
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr	
20 25 30	
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr	
35 40 45	
Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu	
50 55 60	
Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys	
65 70 75 80	
Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly	
85 90 95	
Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe	
100 105 110	
Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr	
115 120 125	
Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu	
130 135 140	
His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro	
145 150 155 160	
Leu Asn Ser Arg Ala Val Glu Asp Ile Ser Ser Ser Arg Thr Asn Pro	
165 170 175	
Tyr Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe Leu Thr Tyr His	
180 185 190	
Met Trp Pro Leu Thr Phe Leu Ser Pro Ser Glu Leu Ala Arg Ala Gly	
195 200 205	
Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys Gly	
210 215 220	
Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp Ala Met Ser Glu His	
225 230 235 240	

Arg Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Glu Thr
 245 250 255
 Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Ala Arg
 260 265 270
 Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu
 275 280 285
 Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp Asp Val
 290 295 300
 Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser Gly Asp
 305 310 315 320
 Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu Phe Leu
 325 330 335
 Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile Gln Gly Arg Tyr
 340 345 350
 Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Thr Thr Gly Glu
 355 360 365
 Glu Asn Ala Asp Pro Pro Ile Ile His Phe Gly Pro Gly Glu Ser Ser
 370 375 380
 Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
 385 390 395 400
 Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Gln Ser Lys
 405 410 415
 Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
 420 425 430
 Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Lys Glu Lys
 435 440 445
 Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
 450 455 460
 Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
 465 470 475 480
 Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
 485 490 495
 Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
 500 505 510
 Ile Leu Val Lys Gly Asn Ala Ala Asn Ile Phe Lys Asn Cys Leu
 515 520 525
 Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
 530 535 540
 Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
 545 550 555 560
 Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
 565 570 575
 Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys
 580 585 590

Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Gly	Ile
595						600					605				
<hr/>															
Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser						
610					615										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCAGCAGG	TTTACAAAGG	AGGAAAACGA	CTTCTTCTAG	ATTTTTTTTT	CAGTTTCTTC	60
TATAAATCAA	AACTACCTCC	CTAGAGAAAG	GCTAGTCCCT	TTTCTTCCCC	ATTCAATTCA	120
TTATGAACAT	AGTAGAAAAAC	AGCATATTCT	TATCAAATT	GATGAAAAGC	GCCAACACGT	180
TTGAACTGAA	ATACGACTTG	TCATGTGAAC	TGTACCGAAT	GTCTACGTAT	TCCACTTTTC	240
CTGCTGGGGT	CCCTGTCTCA	GAAAGGAGTC	TTGCTCGCGC	TGGTTTCTAT	TACACTGGTG	300
TGAATGACAA	GGTCAAATGC	TTCTGTTGTG	GCCTGATGCT	GGATAACTGG	AAAAGAGGAG	360
ACAGTCCTAC	TGAAAAGCAT	AAAAAGTTGT	ATCCTAGCTG	CAGATTGTT	CAGAGTCTAA	420
ATTCCGTTAA	CAACTTGAA	GCTACCTCTC	AGCCTACTTT	TCCTTCTTC	GTAACAAATT	480
CCACACACTC	ATTACTTCCG	GGTACAGAAA	ACAGTGGATA	TTTCCGTGGC	TCTTATTCAA	540
ACTCTCCATC	AAATCCTGTA	AACTCCAGAG	CAAATCAAGA	TTTTTCTGCC	TTGATGAGAA	600
GTT CCTACCA	CTGTGCAATG	AATAACGAAA	ATGCCAGATT	ACTTACTTTT	CAGACATGGC	660
CATTGACTTT	TCTGTCGCCA	ACAGATCTGG	CAAAGCAGG	CTTTTACTAC	ATAGGACCTG	720
GAGACAGAGT	GGCTTGCTTT	GCCTGTGGTG	GAAAATTGAG	CAATTGGAA	CCGAAGGATA	780
ATGCTATGTC	AGAACACCTG	AGACATTTC	CCAAATGCC	ATTTATAGAA	AATCAGCTTC	840
AAGACACTTC	AAGATAACACA	GTTTCTAATC	TGAGCATGCA	GACACATGCA	GCCCGCTTTA	900
AAACATTCTT	AAACTGGCCC	TCTAGTGTTC	TAGTTAATCC	TGAGCAGCTT	GCAAGTGC GG	960
GT TTTTATTA	TGTGGTAAC	AGTGTATGATG	TCAAATGCTT	TTGCTGTGAT	GGTGGACTCA	1020
GGTGTGTTGGGA	ATCTGGAGAT	GATCCATGGG	TTCAACATGC	CAA GTGGTTT	CCAAGGTGTG	1080
AGTACTTGAT	AAGAATTAAG	GGACAGGAGT	TCATCCGTCA	AGTTCAAGCC	AGTTACCCTC	1140
ATCTACTTGA	ACAGCTGCTA	TCCACATCAG	ACAGCCCAGG	AGATGAAAAT	GCAGAGTCAT	1200
CAATTATCCA	TTTTGAACCT	GGAGAAAGACC	ATTCAGAAGA	TGCAATCATG	ATGAATACTC	1260
CTGTGATTAA	TGCTGCCGTG	GAAATGGGCT	TTAGTAGAAG	CCTGGTAAAA	CAGACAGTTC	1320
AGAGAAAAAT	CCTAGCAACT	GGAGAGAATT	ATAGACTAGT	CAATGATCTT	GTGTTAGACT	1380
TACTCAATGC	AGAAGATGAA	ATAAGGGAAG	AGGAGAGAGA	AAGAGCAACT	GAGGAAAAAG	1440

AATCAAATGA TTTATTATTA ATCCGGAAGA ATAGAACGGC ACTTTTCAA CATTGACTT	1500
G TGTAATTCC AATCCTGGAT AGTCTACTAA CTGCCGGAAT TATTAATGAA CAAGAACATG	1560
ATGTTATTAA ACAGAAGACA CAGACGTCTT TACAAGCAAG AGAACTGATT GATACGATTT	1620
TAGTAAAAGG AAATATTGCA GCCACTGTAT TCAGAAACTC TCTGCAAGAA GCTGAAGCTG	1680
TGTTATATGA GCATTTATT GTGCAACAGG ACATAAAATA TATTCCCACA GAAGATGTTT	1740
CAGATCTACC AGTGGAAAGAA CAATTGCGGA GACTACAAGA AGAAAGAACAGTAAAGTGT	1800
GTATGGACAA AGAAGTGTCC ATAGTGTAA TTCCTTGAG TCATCTAGTA GTATGCAAAG	1860
ATTGTGCTCC TTCTTTAAGA AAGTGTCTA TTTGTAGGAG TACAATCAAG GGTACAGTT	1920
GTACATTTCTTTCATGAAGA AGAACCAAAA CATCATCTAA ACTTTAGAAT TAATTTATTA	1980
AATGTATTAT AACTTTAACT TTCACTCTAA TTGGTTTCC TTAAAATTTT TATTTATTA	2040
CAACTCAACA AACATTGTT TGTGTACAT ATTTAATATA TGTATCTAAA CCATATGAAC	2100
ATATATTTTT TAGAAACTAA GAGAATGATA GGCTTTGTT CTTATGAACG AAAAGAGGT	2160
AGCACTACAA ACACAATATT CAATCAAAAT TTCAAGCATTAA TTGAAATTGT AAGTGAAGTA	2220
AAACTTAAGA TATTTGAGTT AACCTTAAG AATTTAAAT ATTTTGGCAT TGTACTAATA	2280
CCGGGAACAT GAAGCCAGGT GTGGTGTAT GTGCCTGTAG TCCCAGGCTG AGGCAAGAGA	2340
ATTACTTGAG CCCAGGAGTT TGAATCCATC CTGGGCAGCA TACTGAGACC CTGCCTTTAA	2400
AAACAAACAG AACAAAAACAA AACACCCAGG GACACATTTC TCTGTCTTTT TTGATCAGTG	2460
TCCTATACAT CGAAGGTGTG CATATATGTT GAATGACATT TTAGGGACAT GGTGTTTTA	2520
TAAAGAATTC TGTGAGAAAA AATTTAATAA AACCCCCCAA ATTAAAAAAA AAAAAAAAAA	2580
AAAAAAAAAAA AAAAAAAAAA A	2601

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser	
1 5 10 15	

Ala Asn Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg	
20 25 30	

Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg	
35 40 45	

Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val	
50 55 60	

Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp	
65 70 75 80	

Ser	Pro	Thr	Glu	Lys	His	Lys	Leu	Tyr	Pro	Ser	Cys	Arg	Phe	Val	
				85			90					95			
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Gln	Ser	Leu	Asn	Ser	Val	Asn	Asn	Leu	Glu	Ala	Thr	Ser	Gln	Pro	Thr
		100				105						110			
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Phe	Pro	Ser	Ser	Val	Thr	Asn	Ser	Thr	His	Ser	Leu	Leu	Pro	Gly	Thr
	115					120						125			
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Glu	Asn	Ser	Gly	Tyr	Phe	Arg	Gly	Ser	Tyr	Ser	Asn	Ser	Pro	Ser	Asn
	130				135						140				
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Pro	Val	Asn	Ser	Arg	Ala	Asn	Gln	Asp	Phe	Ser	Ala	Leu	Met	Arg	Ser
	145				150			155			160				
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Ser	Tyr	His	Cys	Ala	Met	Asn	Asn	Glu	Asn	Ala	Arg	Leu	Leu	Thr	Phe
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Gln	Thr	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Thr	Asp	Leu	Ala	Lys	Ala
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Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys
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Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asn	Ala	Met	Ser	Glu
	210				215			220							
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His	Leu	Arg	His	Phe	Pro	Lys	Cys	Pro	Phe	Ile	Glu	Asn	Gln	Leu	Gln
	225				230			235			240				
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Asp	Thr	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala
	245				250			255							
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Ala	Arg	Phe	Lys	Thr	Phe	Phe	Asn	Trp	Pro	Ser	Ser	Val	Leu	Val	Asn
	260				265			270							
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Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Asn	Ser	Asp
	275				280			285							
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Asp	Val	Lys	Cys	Phe	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser
	290				295			300							
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Gly	Asp	Asp	Pro	Trp	Val	Gln	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu
	305				310			315			320				
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Tyr	Leu	Ile	Arg	Ile	Lys	Gly	Gln	Glu	Phe	Ile	Arg	Gln	Val	Gln	Ala
	325				330			335							
<hr/>															
Ser	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Ser	Pro
	340				345			350							
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Gly	Asp	Glu	Asn	Ala	Glu	Ser	Ser	Ile	Ile	His	Phe	Glu	Pro	Gly	Glu
	355				360			365							
<hr/>															
Asp	His	Ser	Glu	Asp	Ala	Ile	Met	Met	Asn	Thr	Pro	Val	Ile	Asn	Ala
	370				375			380							
<hr/>															
Ala	Val	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Lys	Gln	Thr	Val	Gln
	385			390			395					400			
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Arg	Lys	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Leu	Val	Asn	Asp	Leu
	405					410					415				
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Val	Leu	Asp	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Ile	Arg	Glu	Glu	Glu	Arg
	420					425					430				

Glu	Arg	Ala	Thr	Glu	Glu	Lys	Glu	Ser	Asn	Asp	Leu	Leu	Leu	Ile	Arg
435							440							445	
<hr/>															
Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Ile	Pro	Ile
450					455						460				
Leu	Asp	Ser	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Asn	Glu	Gln	Glu	His	Asp
465					470					475				480	
Val	Ile	Lys	Gln	Lys	Thr	Gln	Thr	Ser	Leu	Gln	Ala	Arg	Glu	Leu	Ile
					485				490				495		
Asp	Thr	Ile	Leu	Val	Lys	Gly	Asn	Ile	Ala	Ala	Thr	Val	Phe	Arg	Asn
							500		505				510		
Ser	Leu	Gln	Glu	Ala	Glu	Ala	Val	Leu	Tyr	Glu	His	Leu	Phe	Val	Gln
							515		520			525			
Gln	Asp	Ile	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Asp	Leu	Pro	Val
					530			535			540				
Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys
					545			550		555				560	
Met	Asp	Lys	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val
					565				570				575		
Val	Cys	Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg
					580				585				590		
Ser	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser				
					595				600						

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys	Glu	Leu	Tyr	Arg	Met	Ser	Thr	Thr	Ser	Thr	Phe	Pro	Ala	Gly	Val
1					5						10				15
Pro	Val	Ser	Glu	Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly
						20				25			30		
Val	Asn	Asp	Lys	Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn
						35			40			45			
Trp	Lys	Leu	Gly	Asp	Ser	Pro									
					50				55						

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Glu	Leu	Tyr	Arg	Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val
1					5				10					15	
Pro	Val	Ser	Glu	Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly
	20							25				30			
Val	Asn	Asp	Lys	Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn
	35					40				45					
Trp	Lys	Arg	Gly	Asp	Ser	Pro									
	50				55										

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala
1					5				10				15		
Cys	Phe	Ala	Cys	Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp
	20					25					30				
Ala	Met	Ser	Glu	His	Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe		
	35					40					45				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Ala	Lys	Ala	Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala
1					5				10				15		
Cys	Phe	Ala	Cys	Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asn
	20					25					30				
Ala	Met	Ser	Glu	His	Leu	Arg	His	Phe	Pro	Lys	Cys	Pro	Phe		
	35					40					45				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp
1 5 10 15
Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
20 25 30
Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
1 5 10 15
Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
20 25 30
Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Glu Arg Thr Cys Lys Val Cys Met Asp Lys Glu Val Ser Val Val
1 5 10 15
Phe Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser
20 25 30
Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile Ile Lys Gly Thr Val Arg
35 40 45
Thr Phe Leu Ser
50

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met	Asp	Lys	Glu	Val	Ser	Ile	Val
1				5				10						15	

Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val	Cys	Lys	Asp	Cys	Ala	Pro	Ser
					20			25					30		

Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Ser	Thr	Ile	Lys	Gly	Thr	Val	Arg
					35			40				45			

Thr	Phe	Leu	Ser
		50	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCCTTACA	GTGAATACTG	TAGTCCTAAC	AGACCTGAGC	TGACTGCTGC	AGTTGATGTA	60
ACCCACTTTA	GAGAATACTG	TATGACATCT	TCTCTAAGGA	AAACCAGCTG	CAGACTTCAC	120
TCAGTTCCCTT	TCATTTCATCA	GGAAAAGGAG	TAGTTCAAGAT	GTCATGTTTA	AGTCCTTATA	180
AGGGAAAAGA	GCCTGAATAT	ATGCCCTAGT	ACCTAGGCTT	CATAACTAGT	AATAAGAAGT	240
TAGTTATGGG	TAAATAGATC	TCAGGTTACC	CAGAAGAGTT	CATGTGACCC	CCAAAGAGTC	300
CTAACTAGTG	TCTTGGCAAG	TGAGACAGAT	TTGTCCTGTG	AGGGTGTCAA	TTCACCGAGTC	360
CAAGCAGAAG	ACAATGAATC	TATCCAGTCA	GGTGTCTGTG	GTGGAGATCT	AGTGTCAAGT	420
GGTGAGAAC	TTCATCTGGA	AGTTAACGCG	GTCAGAAATA	CTATTACTAC	TCATGGACAA	480
AACTGTCTCC	CAGAGACTCG	GCCAAGGTAC	CTTACACCAA	AAACTTAAAC	GTATAATGGA	540
GAAGAGCACA	ATCTTGTCAA	ATTGGACAAA	GGAGAGCGAA	GAAAAAATGA	AGTTTGACTT	600
TTCGTGTGAA	CTCTACCGAA	TGTCTACATA	TTCAGCTTTT	CCCAGGGGAG	TTCCCTGTCTC	660
AGAGAGGGAGT	CTGGCTCGTG	CTGGCTTTTA	TTATACAGGT	GTGAATGACA	AAGTCAAGTG	720
CTTCTGCTGT	GGCCTGATGT	TGGATAACTG	GAAACAAGGG	GACAGTCTG	TTGAAAAGCA	780
CAGACAGTTC	TATCCCAGCT	GCAGCTTTGT	ACAGACTCTG	CTTCAGCCA	GTCTGCAGTC	840
TCCCATCTAAG	AATATGTCTC	CTGTGAAAAG	TAGATTTGCA	CATTGTCAC	CTCTGGAACG	900

AGGTGGCATT CACTCCAACC TGTGCTCTAG CCCTCTTAAT TCTAGAGCAG TGGAAGACTT	960
CTCATCAAGG ATGGATCCCT GCAGCTATGC CATGAGTACA GAAGAGGCCA GATTTCCTAC	1020
TTACAGTATG TGGCCTTAA GTTTCTGTC ACCAGCAGAG CTGGCCAGAG CTGGCTTCTA	1080
TTACATAGGG CCTGGAGACA GGGTGGCCTG TTTGCGCTGT GGTGGGAAAC TGAGCAACTG	1140
GGAACCAAAG GATGATGCTA TGTCAGAGCA CCGCAGACAT TTTCCCCACT GTCCATTCT	1200
GGAAAATACT TCAGAACAC AGAGGTTTAG TATATCAAAT CTAAGTATGC AGACACACTC	1260
TGCTCGATTG AGGACATTTC TGTACTGGCC ACCTAGTGTT CCTGTTCAGC CCGAGCAGCT	1320
TGCAAGTGCT GGATTCTATT ACGTGGATCG CAATGATGAT GTCAAGTGCT TTTGTTGTGA	1380
TGGTGGCTTG AGATGTTGGG AACCTGGAGA TGACCCCTGG ATAGAACACG CCAAATGGTT	1440
TCCAAGGTGT GAGTTCTTGA TACGGATGAA GGGTCAGGAG TTTGTTGATG AGATTCAAGC	1500
TAGATATCCT CATCTTCTTG AGCAGCTGTT GTCCACTTCA GACACCCCAAG GAGAAGAAAA	1560
TGCTGACCCCT ACAGAGACAG TGGTGCATTT TGGCCCTGGA GAAAGTTCGG AAGATGTCGT	1620
CATGATGAGC ACGCCTGTGG TTAAAGCAGC CTTGGAAATG GGCTTCAGTA GGAGCCTGGT	1680
GAGACAGACG GTTCAGCGGC AGATCCTGGC CACTGGTGAG AACTACAGGA CCGTCAATGA	1740
TATTGTCCTCA GTACTTTGA ATGCTGAAGA TGAGAGAAGA GAAGAGGAGA AGGAAAGACA	1800
GAECTGAAGAG ATGGCATTCAAG GTGACTTATC ACTGATTTCGG AAGAATAGAA TGGCCCTCTT	1860
TCAACAGTTG ACACATGTCC TTCCTATCCT GGATAATCTT CTTGAGGCCA GTGTAATTAC	1920
AAAACAGGAA CATGATATTA TTAGACAGAA AACACAGATA CCCTTACAAG CAAGAGAGCT	1980
TATTGACACC GTTTTAGTCA AGGGAAATGC TGCAGCCAAC ATCTTCAAAA ACTCTCTGAA	2040
GGAAATTGAC TCCACGTTAT ATGAAAACCTT ATTTGTGGAA AAGAATATGA AGTATATTCC	2100
AACAGAAGAC GTTTCAGGCT TGTCTTGAA AGAGCAGTTG CGGAGATTAC AAGAAGAACG	2160
AACTTGCAAA GTGTGTATGG ACAGAGAGGT TTCTATTGTG TTCATTCCGT GTGGTCATCT	2220
AGTAGTCTGC CAGGAATGTG CCCCTCTCT AAGGAAGTGC CCCATCTGCA GGGGGACAAT	2280
CAAGGGGACT GTGCGCACAT TTCTCTCATG AGTGAAGAAT GGTCTGAAAG TATTGTTGGA	2340
CATCAGAACG TGTCAGAAC AAGAATGAAC TACTGATTTC AGCTCTTCAG CAGGACATTC	2400
TACTCTCTTT CAAGATTAGT AATCTTGCTT TATGAAGGGT AGCATTGTAT ATTAAAGCTT	2460
AGTCTGTTGC AAGGAAAGGT CTATGCTGTT GAGCTACAGG ACTGTGTCTG TTCCAGAGCA	2520
GGAGTTGGGA TGCTTGCTGT ATGTCCTTCA GGACTTCTTG GATTTGGAAT TTGTGAAAGC	2580
TTTGGATTCA GGTGATGTGG AGCTCAGAAA TCCTGAAACC AGTGGCTCTG GTACTCAGTA	2640
GTAGGGTAC CCTGTGCTTC TTGGTGCTTT TCCTTTCTGG AAAATAAGGA TTTTCTGCT	2700
ACTGGTAAAT ATTTTCTGTT TGTGAGAAAT ATATTAAAGT GTTTCTTTA AAGGCGTGCA	2760
TCATTGTAGT GTGTGCAGGG ATGTATGCAG GCAAAACACT GTGTATATAA TAAATAAAATC	2820
TTTTAAAAAA GTGAAAAAAA AAAAAAAA AAAAAAAA AA	2862

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Lys Thr Val Ser Gln Arg Leu Gly Gln Gly Thr Leu Ile His Gln
1 5 10 15

Lys Leu Lys Arg Ile Met Glu Lys Ser Thr Ile Leu Ser Asn Trp Thr
20 25 30

Lys Glu Ser Glu Glu Lys Met Lys Phe Asp Phe Ser Cys Glu Leu Tyr
 35 . 40 45

Arg Met Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro Val Ser Glu
50 55 60

Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
65 70 75 80

Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Gln Gly
85 90 95

Asp Ser Pro Val Glu Lys His Arg Gln Phe Tyr Pro Ser Cys Ser Phe
 100 105 110

Val Gln Thr Leu Leu Ser Ala Ser Leu Gln Ser Pro Ser Lys Asn Met
115 120 125

Ser Pro Val Lys Ser Arg Phe Ala His Ser Ser Pro Leu Glu Arg Gly
130 135 140

Gly Ile His Ser Asn Leu Cys Ser Ser Pro Leu Asn Ser Arg Ala Val
145 150 155 160

Glu Asp Phe Ser Ser Arg Met Asp Pro Cys Ser Tyr Ala Met Ser Ile
165 170 175

Glu Glu Ala Arg Phe Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu
 180 185 190

Ser Pro Ala Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
195 200 205

Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Ile Glu
210 215 220

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro His Cys
225 230 235 240

Pro Phe Leu Glu Asn Thr Ser Glu Thr Gin Arg Phe Ser Ile Ser Asn
245 250 255

Leu Ser Met Gln Thr His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Ile
260 265 270

Pro Pro Ser Val Pro Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe
275 280 285

Tyr Tyr Val Asp Arg Asn Asp Asp Val Lys Cys Phe Cys Cys Asp Gly
 290 295 300
 Gly-Leu-Arg-Gys-Trp-Glu-Pro-Gly-Asp-Asp-Pro-Trp-Ile-Glu-His-Ala
 305 310 315 320
 Lys Trp Phe Pro Arg Cys Glu Phe Leu Ile Arg Met Lys Gly Gln Glu
 325 330 335
 Phe Val Asp Glu Ile Gln Ala Arg Tyr Pro His Leu Leu Glu Gln Leu
 340 345 350
 Leu Ser Thr Ser Asp Thr Pro Gly Glu Glu Asn Ala Asp Pro Thr Glu
 355 360 365
 Thr Val Val His Phe Gly Pro Gly Glu Ser Ser Glu Asp Val Val Met
 370 375 380
 Met Ser Thr Pro Val Val Lys Ala Ala Leu Glu Met Gly Phe Ser Arg
 385 390 395 400
 Ser Leu Val Arg Gln Thr Val Gln Arg Gln Ile Leu Ala Thr Gly Glu
 405 410 415
 Asn Tyr Arg Thr Val Asn Asp Ile Val Ser Val Leu Leu Asn Ala Glu
 420 425 430
 Asp Glu Arg Arg Glu Glu Glu Lys Glu Arg Gln Thr Glu Glu Met Ala
 435 440 445
 Ser Gly Asp Leu Ser Leu Ile Arg Lys Asn Arg Met Ala Leu Phe Gln
 450 455 460
 Gln Leu Thr His Val Leu Pro Ile Leu Asp Asn Leu Leu Glu Ala Ser
 465 470 475 480
 Val Ile Thr Lys Gln Glu His Asp Ile Ile Arg Gln Lys Thr Gln Ile
 485 490 495
 Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr Val Leu Val Lys Gly Asn
 500 505 510
 Ala Ala Ala Asn Ile Phe Lys Asn Ser Leu Lys Glu Ile Asp Ser Thr
 515 520 525
 Leu Tyr Glu Asn Leu Phe Val Glu Lys Asn Met Lys Tyr Ile Pro Thr
 530 535 540
 Glu Asp Val Ser Gly Leu Ser Leu Glu Glu Gln Leu Arg Arg Leu Gln
 545 550 555 560
 Glu Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val
 565 570 575
 Phe Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser
 580 585 590
 Leu Arg Lys Cys Pro Ile Cys Arg Gly Thr Ile Lys Gly Thr Val Arg
 595 600 605
 Thr Phe Leu Ser
 610

WHAT IS CLAIMED IS:

1. An isolated nucleic acid having the sequence defined by SEQUENCE ID NO: 1 or 3, or a fragment thereof capable of specifically hybridizing with a nucleic acid having the sequence defined by SEQUENCE ID NO: 1 or 3 under stringency conditions defined by a hybridization buffer comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M NaPO₄, pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with the 0.2 x SSPE.
- 10 2. An isolated nucleic acid according to claim 1 capable of specifically hybridizing with a nucleic acid having the sequence defined by SEQUENCE ID NO: 1 or 3 under stringency conditions defined by a hybridization buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C.
- 15 3. An isolated nucleic acid according to claim 1 encoding a human cellular inhibitor of apoptosis protein (c-IAP) comprising at least two of: a first domain comprising SEQUENCE ID NO: 5 or 6, a second domain comprising SEQUENCE ID NO: 7 or 8, and a third domain comprising SEQUENCE ID NO: 9 or 10; said protein having a c-IAP specific activity.
- 20 4. A method of making a human cellular inhibitor of apoptosis protein (c-IAP) comprising introducing a nucleic acid according to claim 3 into a host cell, growing said host cell under conditions whereby said nucleic acid is expressed as a transcript and said transcript is expressed as a translation product comprising a cellular inhibitor of apoptosis protein, and isolating said translation product.
- 25 5. A method of identifying lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease, said method comprising the steps of:
 - 30 incubating a mixture comprising:
 - a human c-IAP made by a method according to claim 4,

- a natural intracellular human c-IAP binding target, wherein said binding target is capable of specifically binding said human c-IAP, and a candidate pharmacological agent;
- under conditions whereby, but for the presence of said candidate
- 5 pharmacological agent, said human c-IAP specifically binds said binding target at a reference affinity;
- detecting the binding affinity of said human c-IAP to said binding target to determine an agent-biased affinity,
- wherein a difference between the agent-biased affinity and the test affinity
- 10 indicates that said candidate pharmacological agent is a lead compound for a pharmacological agent capable of modulating human c-IAP-dependent signal transduction.
6. A method according to claim 5, wherein said human c-IAP binding target
- 15 comprises a TRAF or an intracellular fragment of a TRAF sufficient to provide for c-IAP-specific binding.
7. A method of modulating apoptosis regulation in a cell comprising introducing into said cell a nucleic acid according to claim 1 whereby said nucleic acid is
- 20 expressed in said cell and the resultant gene product modulates apoptosis regulation in said cell.
8. A method of modulating apoptosis regulation in a cell comprising introducing into said cell a nucleic acid according to claim 3 whereby said nucleic acid is
- 25 expressed in said cell and the resultant gene product modulates apoptosis regulation in said cell.
9. A method according to claim 8 wherein said cell expresses a recombinant protein in in vitro culture and said gene product inhibits apoptosis in said cell,
- 30 whereby the yield of said recombinant protein is increased.

INTERNATIONAL SEARCH REPORT

<p>International application No. PCT/US96/12860</p>

A. CLASSIFICATION OF SUBJECT-MATTER

IPC(6) :C07H 21/04; C12P 21/00; C12Q 1/00

US CL :435/5, 69.1; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/5, 69.1; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN: Medline, Biosis, CAPlus, WPIDS
apoptosis, iap(s), TRAF(s)**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	ROTHE et al. The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins. Cell. 29 December 1995, Vol.83, pages 1243-1252, see entire document.	1-9
A,P	CLEM et al. Anti-apoptotic genes of baculoviruses. Cell death and differentiation. January 1996, Vol.3, pages 9-16.	1-9
A	ROY et al. The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy. Cell. 13 January 1995, Vol.80, pages 167-178.	1-9

 Further documents are listed in the continuation of Box C. See patent family annex.

- * Special categories of cited documents:
 "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- "&" document member of the same patent family

Date of the actual completion of the international search 11 SEPTEMBER 1996	Date of mailing of the international search report 24 OCT 1996
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Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer ROBERT A. SCHWARTZMAN <i>R. Schwartzman</i>
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/12860

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ROTHE et al. TRAF2-mediated activation of NF-kB by TNF receptor 2 and CD40. Science.08 September 1995, Vol.269, pages 1424-1427.	1-9